RAW SEQUENCE LISTING
PATENT APPLICATION:  US/09/689,730

DATE: 12/11/2001
TIME: 18:17:14

Input Set : **N:\Crf3\RULE60\09689730.raw**
Output Set: **N:\CRF3\12112001\I689730.raw**

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 1 <110> APPLICANT: SEIKI, Motoharu
 2          SATO, Hiroshi
 3          SHINAGAWA, Akira
 4 <120> TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
 5 <130> FILE REFERENCE: 55-290P
 6 <140> CURRENT APPLICATION NUMBER: 09/689,730
 7 <141> CURRENT FILING DATE: 2000-10-13
 8 <150> PRIOR APPLICATION NUMBER: US/08/448,489
 9 <151> PRIOR FILING DATE: 1995-06-07
10 <160> NUMBER OF SEQ ID NOS: 19
11 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 582
15 <212> TYPE: PRT
16 <213> ORGANISM: Homo sapiens
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20      Thr Leu Gly Thr Ala Leu Ala Ser Leu Gly Ser Ala Gln Ser Ser Ser
21                      20                  25                  30
22      Phe Ser Pro Glu Ala Trp Leu Gln Gln Tyr Gly Tyr Leu Pro Pro Gly
23                  35                  40                  45
24      Asp Leu Arg Thr His Thr Gln Arg Ser Pro Gln Ser Leu Ser Ala Ala
25          50                  55                  60
26      Ile Ala Ala Met Gln Lys Phe Tyr Gly Leu Gln Val Thr Gly Lys Ala
27          65                  70                  75                  80
28      Asp Ala Asp Thr Met Lys Ala Met Arg Arg Pro Arg Cys Gly Val Pro
29                      85                  90                  95
30      Asp Lys Phe Gly Ala Glu Ile Lys Ala Asn Val Arg Arg Lys Arg Tyr
31                     100                 105                 110
32      Ala Ile Gln Gly Leu Lys Trp Gln His Asn Glu Ile Thr Phe Cys Ile
33                     115                 120                 125
34      Gln Asn Tyr Thr Pro Lys Val Gly Glu Tyr Ala Thr Tyr Glu Ala Ile
35                     130                 135                 140
36      Arg Lys Ala Phe Arg Val Trp Glu Ser Ala Thr Pro Leu Arg Phe Arg
37          145                 150                 155                 160
38      Glu Val Pro Tyr Ala Tyr Ile Arg Glu Gly His Glu Lys Gln Ala Asp
39                     165                 170                 175
40      Ile Met Ile Phe Phe Ala Glu Gly Phe His Gly Asp Ser Thr Pro Phe
41                     180                 185                 190
42      Asp Gly Glu Gly Gly Phe Leu Ala His Ala Tyr Phe Pro Gly Pro Asn
43                     195                 200                 205
44      Ile Gly Gly Asp Thr His Phe Asp Ser Ala Glu Pro Trp Thr Val Arg
45          210                 215                 220
46      Asn Glu Asp Leu Asn Gly Asn Asp Ile Phe Leu Val Ala Val His Glu
47          225                 230                 235                 240
48      Leu Gly His Ala Leu Gly Leu Glu His Ser Ser Asp Pro Ser Ala Ile
```

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 49                              245                   250                        255
 50        Met Ala Pro Phe Tyr Gln Trp Met Asp Thr Glu Asn Phe Val Leu Pro
 51                              260                   265                   270
 52        Asp Asp Asp Arg Arg Gly Ile Gln Gln Leu Tyr Gly Gly Glu Ser Gly
 53                         275                   280                   285
 54        Phe Pro Thr Lys Met Pro Pro Gln Pro Arg Thr Thr Ser Arg Pro Ser
 55                    290                   295                   300
 56        Val Pro Asp Lys Pro Lys Asn Pro Thr Tyr Gly Pro Asn Ile Cys Asp
 57        305                   310                   315                   320
 58        Gly Asn Phe Asp Thr Val Ala Met Leu Arg Gly Glu Met Phe Val Phe
 59                         325                   330                   335
 60        Lys Lys Arg Trp Phe Trp Arg Val Arg Asn Asn Gln Val Met Asp Gly
 61                    340                   345                   350
 62        Tyr Pro Met Pro Ile Gly Gln Phe Trp Arg Gly Leu Pro Ala Ser Ile
 63              355                   360                   365
 64        Asn Thr Ala Tyr Glu Arg Lys Asp Gly Lys Phe Val Phe Phe Lys Gly
 65        370                   375                   380
 66        Asp Lys His Trp Val Phe Asp Glu Ala Ser Leu Glu Pro Gly Tyr Pro
 67        385                   390                   395                   400
 68        Lys His Ile Lys Glu Leu Gly Arg Gly Leu Pro Thr Asp Lys Ile Asp
 69                         405                   410                   415
 70        Ala Ala Leu Phe Trp Met Pro Asn Gly Lys Thr Tyr Phe Phe Arg Gly
 71                    420                   425                   430
 72        Asn Lys Tyr Tyr Arg Phe Asn Glu Glu Leu Arg Ala Val Asp Ser Glu
 73              435                   440                   445
 74        Tyr Pro Lys Asn Ile Lys Val Trp Glu Gly Ile Pro Glu Ser Pro Arg
 75        450                   455                   460
 76        Gly Ser Phe Met Gly Ser Asp Glu Val Phe Thr Tyr Phe Tyr Lys Gly
 77        465                   470                   475                   480
 78        Asn Lys Tyr Trp Lys Phe Asn Asn Gln Lys Leu Lys Val Glu Pro Gly
 79                         485                   490                   495
 80        Tyr Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser Gly Gly
 81                    500                   505                   510
 82        Arg Pro Asp Glu Gly Thr Glu Glu Glu Thr Glu Val Ile Ile Ile Glu
 83              515                   520                   525
 84        Val Asp Glu Glu Gly Gly Gly Ala Val Ser Ala Ala Ala Val Val Leu
 85        530                   535                   540
 86        Pro Val Leu Leu Leu Leu Leu Val Leu Ala Val Gly Leu Ala Val Phe
 87        545                   550                   555                   560
 88        Phe Phe Arg Arg His Gly Thr Pro Arg Arg Leu Leu Tyr Cys Gln Arg
 89                    565                   570                   575
 90        Ser Leu Leu Asp Lys Val
 91                    580
 93   <210> SEQ ID NO: 2
 94   <211> LENGTH: 3403
 95   <212> TYPE: DNA
 96   <213> ORGANISM: Homo sapiens
 97   <400> SEQUENCE: 2
 98        agttcagtgc ctaccgaaga caaaggcgcc ccgagggagt ggcggtgcga ccccagggcg 60
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Input Set : N:\Crf3\RULE60\09689730.raw
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100    gccccaagac cctcccgttg tctcctgctc cccctgctca cgctcggcac cgcgctcgcc 180
101    tccctcggct cggcccaaag cagcagcttc agccccgaag cctggctaca gcaatatggc 240
102    tacctgcctc ccggggacct acgtacccac acacagcgct caccccagtc actctcagcg 300
103    gccatcgctg ccatgcagaa gttttacggc ttgcaagtaa caggcaaagc tgatgcagac 360
104    accatgaagg ccatgaggcg cccccgatgt ggtgttccag acaagtttgg ggctgagatc 420
105    aaggccaatg ttcgaaggaa gcgctacgcc atccagggtc tcaaatggca acataatgaa 480
106    attactttct gcatccagaa ttacaccccc aaggtgggcg agtatgccac atacgaggcc 540
107    attcgcaagg cgttccgcgt gtgggagagt gccacaccac tgcgcttccg cgaggtgccc 600
108    tatgcctaca tccgtgaggg ccatgagaag caggccgaca tcatgatctt ctttgccgag 660
109    ggcttccatg cgcacagcac gcccttcgat ggtgagggcg gcttcctggc ccatgcctac 720
110    ttcccagggc ccaacattgg aggagacacc cactttgact ctgccgagcc ttggactgtc 780
111    aggaatgagg atctgaatgg aaatgacatc ttcctggtgg ctgtgcacga gctgggccat 840
112    gccctggggc tcgagcattc cagtgacccc tcggccatca tggcaccctt ttaccagtgg 900
113    atggacacgg agaattttgt gcttcccgat gatgaccgcc ggggcatcca gcaactttat 960
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115    tctgttcctg ataaacccaa aaaccccacc tatgggccca acatctgtga cgggaacttt 1080
116    gacaccgtgg ccatgctccg aggggagatg tttgtcttca agaagcgctg gttctggcgg 1140
117    gtgaggaata accaagtgat ggatggatac ccaatgccca ttggccagtt ctggcggggc 1200
118    ctgcctgcgt ccatcaacac tgcctacgag aggaaggatg gcaaattcgt cttcttcaaa 1260
119    ggagacaagc attgggtgtt tgatgaggcg tccctggaac ctggctaccc caagcacatt 1320
120    aaggagctgg gccgagggct gcctaccgac aagattgatg ctgctctctt ctggatgccc 1380
121    aatggaaaga cctacttctt ccgtggaaac aagtactacc gtttcaacga agagctcagg 1440
122    gcagtggata gcgagtaccc caagaacatc aaagtctggg aagggatccc tgagtctccc 1500
123    agagggtcat tcatgggcag cgatgaagtc ttcacttact tctacaaggg gaacaaatac 1560
124    tggaaattca acaaccagaa gctgaaggta gaaccgggct accccaagtc agccctgagg 1620
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128    cgccatggga cccccaggcg actgctctac tgccagcgtt ccctgctgga caaggtctga 1860
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131    gcttctctct gtcccctggc tggcctcctt caccctgacc gcctccctcc ctcctgcccc 2040
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134    tggggctct gcacttgaag gcaggaccct cagacctcgc tggtaaaggt caaatggggt 2220
135    catctgctcc ttttccatcc cctgacatac cttaacctct gaactctgac ctcaggaggc 2280
136    tctgggaac tccagccctg aaagccccag gtgtacccaa ttggcagcct ctcactactc 2340
137    tttctggcta aaaggaatct aatcttgttg agggtagaga ccctgagaca gtgtgagggg 2400
138    gtggggactg ccaagccacc ctaagacctt gggaggaaaa ctcagagagg gtcttcgttg 2460
139    ctcagtcagt caagttcctc ggagatcttc ctctgcctca cctaccccag ggaacttcca 2520
140    aggaaggagc ctgagccact ggggactaag tgggcagaag aaaccttgg cagccctgtg 2580
141    cctctcgaat gttagccttg gatgggctt tcacagttag aagagctgaa accaggggtg 2640
142    cagctgtcag gtagggtggg gccggtggga gaggcccggg tcagagccct ggggggtgagc 2700
143    cttaaggcca cagagaaaga accttgccca aactcaggca gctggggctg aggcccaaag 2760
144    gcagaacagc cagaggggc aggaggggac caaaaggaa aatgaggacg tgcagcagca 2820
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147    gctgcccagg cagggtggag gggaagggta gggcagccag agaaaggagc agagaaggca 3000
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```
148        cacaaacgag gaatgagggg cttcacgaga ggccacaggg cctggctggc cacgctgtcc 3060
149        cggcctgctc accatctcag tgagggacag gagctggggc tgcttaggct gggtccacgc 3120
150        ttccctggtg ccagcacccc tcaagcctgt ctcaccagtg gcctgccctc tcgctccccc 3180
151        acccagccca cccattgaag tctccttggg tcccaaaggt gggcatggta ccggggactt 3240
152        gggagagtga gacccagtgg agggagcaag aggagaggga tgtggggggg tggggcacgg 3300
153        gtaggggaaa tggggtgaac ggtgctggca gttcggctag atttctgtct tgtttgtttt 3360
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157 <211> LENGTH: 7
158 <212> TYPE: PRT
159 <213> ORGANISM: Unknown
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Unknown Organism: Highly conserved
162       sequence fragments from MMP family
163 <400> SEQUENCE: 3
164       Pro Arg Cys Gly Val Pro Asp
165           1               5
167 <210> SEQ ID NO: 4
168 <211> LENGTH: 9
169 <212> TYPE: PRT
170 <213> ORGANISM: Unknown
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Description of Unknown Organism: Highly conserved
173       sequence fragments from MMP family
174 <400> SEQUENCE: 4
175       Gly Asp Ala His Phe Asp Asp Asp Glu
176           1               5
178 <210> SEQ ID NO: 5
179 <211> LENGTH: 20
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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187 <210> SEQ ID NO: 6
188 <211> LENGTH: 25
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
193 <400> SEQUENCE: 6
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196 <210> SEQ ID NO: 7
197 <211> LENGTH: 30
198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 7
201       Gly Gly Gly Ala Val Ser Ala Ala Ala Val Val Leu Pro Val Leu Leu
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Input Set : N:\Crf3\RULE60\09689730.raw
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```
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203         Leu Leu Leu Val Leu Ala Val Gly Leu Ala Val Phe Phe Phe
204                     20              25              30
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207 <211> LENGTH: 14
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
210 <400> SEQUENCE: 8
211         Arg Glu Val Pro Tyr Ala Tyr Ile Arg Glu Gly His Glu Lys
212           1           5              10
214 <210> SEQ ID NO: 9
215 <211> LENGTH: 14
216 <212> TYPE: PRT
217 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 9
219         Asp Gly Asn Phe Asp Thr Val Ala Met Leu Arg Gly Glu Met
220           1           5              10
222 <210> SEQ ID NO: 10
223 <211> LENGTH: 15
224 <212> TYPE: PRT
225 <213> ORGANISM: Homo sapiens
226 <400> SEQUENCE: 10
227         Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser Gly Gly
228           1           5              10              15
230 <210> SEQ ID NO: 11
231 <211> LENGTH: 489
232 <212> TYPE: PRT
233 <213> ORGANISM: Unknown
234 <220> FEATURE:
235 <223> OTHER INFORMATION: X = UNKNOWN
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Description of Unknown Organism: Known Member of
238       Matrix Metalloproteinase Family
239 <400> SEQUENCE: 11
240         Met Ala Pro Ala Ala Trp Leu Arg Ser Ala Ala Ala Arg Ala Leu Leu
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242         Pro Pro Met Leu Leu Leu Leu Leu Gln Pro Pro Pro Leu Leu Ala Arg
243                     20              25              30
244         Ala Leu Pro Pro Asp Val His His Leu His Ala Glu Arg Arg Gly Pro
245                     35              40              45
246         Gln Pro Trp His Ala Ala Leu Pro Ser Ser Pro Ala Pro Ala Pro Ala
247                     50              55              60
248         Thr Gln Glu Ala Pro Arg Pro Ala Ser Ser Leu Arg Pro Pro Arg Cys
249           65                70              75              80
250         Gly Val Pro Asp Pro Ser Asp Gly Leu Ser Ala Arg Asn Arg Gln Lys
251                     85              90              95
252         Arg Phe Val Leu Ser Gly Gly Arg Trp Glu Lys Thr Asp Leu Thr Tyr
253                     100             105             110
254         Arg Ile Leu Arg Phe Pro Trp Gln Leu Val Gln Glu Gln Val Arg Gln
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**VERIFICATION SUMMARY**
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Input Set : **N:\Crf3\RULE60\09689730.raw**
Output Set: **N:\CRF3\12112001\I689730.raw**

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L:300 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:440 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:440 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:679 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:679 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
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